

SEQUENCE LISTING

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<120> SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)

<130> 28967/35255A

<140>

<141>

<150> PCT/US99/06133

<151> 1999-03-26

<160> 28

<170> PatentIn Ver. 2.0

<210> 1

<211> 4111

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (20)..(4111)

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Arg	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile	805	810	815	
Met	Asp	Pro	Gly	Glu	Val	Pro	Leu	Glu	Glu	Gln	Cys	Glu	Tyr	Leu	Ser	820	825	830	
Tyr	Asp	Ala	Ser	Gln	Trp	Glu	Phe	Pro	Arg	Glu	Arg	Leu	His	Leu	Gly	835	840	845	
Arg	Val	Leu	Gly	Tyr	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Ser	Ala	850	855	860	
Phe	Gly	Ile	His	Lys	Gly	Ser	Ser	Cys	Asp	Thr	Val	Ala	Val	Lys	Met	865	870	875	880
Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	885	890	895	

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Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser
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Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp
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Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn
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Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly
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Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr
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Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
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Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His
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Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly
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Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser
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Asn Ser Tyr

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ccaccctgc ccccgccagc ggaccggtcc cccacccccg gtccttcac c atg cac 357
Met His
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ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
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Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
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gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
85 90 95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
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Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115 120 125 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
135 140 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
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ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg 885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
165 170 175

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Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
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Ser

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35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
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His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
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tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360

gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
Met Tyr
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Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
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tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
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gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
55 60 65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656
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70 75 80

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cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
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135 140 145

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Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
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Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
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Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
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Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
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Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
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Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
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Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80
Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95
Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
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115 120 125
Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
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Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Thr Trp Pro Gly Ala
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Gln Glu Val Leu Thr Thr Gly Gly Lys Asp Ser Glu Asp Thr Arg Val
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Val His Asp Cys Glu Gly Thr Glu Ala Arg Pro Tyr Cys Lys Val Leu
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Leu Leu Ala Gln Thr His Ala Asn Asn Thr Gly Ser Tyr His Cys Tyr
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Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Thr
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Tyr Val Phe Val Arg Asp Phe Lys His Pro Phe Ile Asn Lys Pro Asp
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Thr Leu Leu Val Asn Arg Lys Asp Ser Met Trp Val Pro Cys Leu Val
145 150 155 160

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675					680					685						
Val	Asn	Val	Ser	Asp	Ser	Leu	Glu	Met	Arg	Cys	Pro	Val	Ala	Gly	Ala	
690					695					700						
His	Val	Pro	Ser	Ile	Val	Trp	Tyr	Lys	Asp	Glu	Arg	Leu	Leu	Glu	Lys	
705					710					715			720			
Glu	Ser	Gly	Ile	Asp	Leu	Ala	Asp	Ser	Asn	Gln	Arg	Leu	Ser	Ile	Gln	
			725					730					735			

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
1025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Ile Val Lys Ile Cys Asp Phe
1045 1050 1055

Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
1060 1065 1070

Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp
1075 1080 1085

Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
1090 1095 1100

Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile
1105 1110 1115 1120

Asn Glu Glu Phe Cys Gln Arg Leu Lys Asp Gly Thr Arg Met Arg Ala
1125 1130 1135

Pro Glu Leu Ala Thr Pro Ala Ile Arg His Ile Met Gln Ser Cys Trp
1140 1145 1150

Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Asp Leu Val Glu Ile
1155 1160 1165

Leu Gly Asp Leu Leu Gln Gly Gly Gly Trp Gln Glu Glu Glu Glu
1170 1175 1180

Arg Met Ala Leu His Ser Ser Gln Ser Ser Glu Glu Asp Gly Phe Met
1185 1190 1195 1200

Gln Ala Ser Thr Thr Ala Leu His Ile Thr Glu Ala Asp Ala Asp Asp
1205 1210 1215

Ser Pro Pro Ser Met His Cys His Ser Leu Ala Ala Arg Tyr Tyr Asn
1220 1225 1230

Cys Val Ser Phe Pro Gly Arg Leu Ala Arg Gly Thr Lys Thr Pro Gly
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Leu Pro Met Thr Pro Thr Thr
1250 1255 1260

Tyr Lys Ala Ser Met Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
1265 1270 1275 1280

Ser Glu Glu Phe Glu Glu Leu Glu Ser Arg His Arg Pro Glu Gly Ser
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln His Met Asp Ile Pro Arg Gly His
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